



SEQUENCE LISTING

<110> DEBBRAH, KNUTZON
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<120> Methods and Compositions for Synthesis of Long Chain Polyunsaturated Fatty Acids

<130> CGAB-210 USA

<140> US 09/367,013

<141> 1999-08-05

<150> US 08/834,655

<151> 1997-04-11

<160> 40

<170> PatentIn version 3.0

<210> 1

<211> 1617

<212> DNA

<213> Mortierella alpina

<220>

<221> misc_feature

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<223> Description of Combined DNA/RNA Molecule: Delta-6 Desaturase Nucleic Acid Sequence

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tgccgaggct ctgaatgagg gcaagaagga tgccgaggca cccttcttga tgatcatcga 180
caacaaggta tacatgttcc gcgagttcgt ccctgatcat cccgggtggaa gtgtgattct 240
cacgcacgtt ggcaaggacg gcactgacgt ctttgacact ttccaccccg aggctgctt 300
ggagactctt gccaactttt acgttggtga tattgacgag agcgaccgcg atatcaagaa 360
tcatgacttt gcggccgagg tccgcaagct gcgtacccctg ttccagtcgtc ttggttacta 420
cgattcttcc aaggcatact acgccttcaa ggtctcggtc aacctctgca tctggggttt 480
gtcgacggtc attgtggcca agtggggcca gacctcgacc ctcgccaacg tgctctcgcc 540
tgcgctttt ggtctgttct ggcagcagtg cgatggttg gtcacgact ttttgcata 600
ccaggtcttc caggaccgtt tctggggta tctttcggc gccttcttgg gaggtgtctg 660
ccagggttcc tcgtcctcgtt ggtggaaagga caagcacaac actcaccacg ccggcccaa 720

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|------|
| cgtccacggc | gaggatcccc | acattgacac | ccaccctctg | ttgacctgga | gtgagcatgc | 780 |
| gttggagatg | ttctcgatg | tcccagatga | ggagctgacc | cgcattgtgt | cgcgttcat | 840 |
| ggtcctgaac | cagacctggt | tttacttccc | cattctctcg | tttgcccgtc | tctcctggtg | 900 |
| cctccagtc | attctctttg | tgctgcctaa | cggtcaggcc | cacaagccct | cgggcgcgcg | 960 |
| tgtgcccata | tcgttggatcg | agcagctgtc | gcttgcgatg | cactggacct | ggtacctcgc | 1020 |
| caccatgttc | ctgttcatca | aggatcccgt | caacatgctg | gtgtactttt | tggtgtcgca | 1080 |
| ggcggtgtgc | ggaaacttgt | tggcgatcgt | gttctcgctc | aaccacaacg | gtatgcctgt | 1140 |
| gatctcgaag | gaggaggcgg | tcgatatgga | tttcttcacg | aaggagatca | tcacgggtcg | 1200 |
| tgatgtccac | ccgggtctat | ttgccaactg | gttcacgggt | ggattgaact | atcagatcga | 1260 |
| gcaccacttg | ttcccttcga | tgcctcgcca | caactttca | aagatccagc | ctgctgtcga | 1320 |
| gaccctgtgc | aaaaagtaca | atgtccgata | ccacaccacc | ggtatgatcg | aggaaactgc | 1380 |
| agaggtcttt | agccgtctga | acgaggtctc | caaggctgcc | tccaagatgg | gtaaggcgca | 1440 |
| gtaaaaaaaaa | aaacaaggac | gtttttttc | gccagtgct | gtgcctgtgc | ctgcttccct | 1500 |
| tgtcaagtcg | agcgttctg | gaaaggatcg | ttcagtgcag | tatcatcatt | ctcctttac | 1560 |
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<210> 2
 <211> 457
 <212> PRT
 <213> Mortierella alpina

<400> 2

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Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
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Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
 35 40 45

Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
 50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
 65 70 75 80

Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
 85 90 95

Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
 100 105 110

Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
 115 120 125

Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
130 135 140

Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
145 150 155 160

Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
180 185 190

Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
195 200 205

His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
210 215 220

Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
225 230 235 240

Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
245 250 255

Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
260 265 270

Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
275 280 285

Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
290 295 300

Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
305 310 315 320

Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
325 330 335

Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His
340 345 350

Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
355 360 365

Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
370 375 380

Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
385 390 395 400

Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
405 410 415

Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
420 425 430

Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
435 440 445

Ala Ala Ser Lys Met Gly Lys Ala Gln
450 455

<210> 3
<211> 1488
<212> DNA
<213> Mortierella alpina

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| ccacccgtctc tcctccaccc tccgagacga ctgcaactgt aatcaggaac cgacaaatac | 120 |
| acgatttctt tttactcagc accaactcaa aatcctcaac cgcaaccctt tttcaggatg | 180 |
| gcacccctcca acactatcga tgccggttt acccagcgtc atatcagcac ctcggcccc | 240 |
| aactcggcca agcctgcctt cgagcgcaac taccagctcc ccgagttcac catcaaggag | 300 |
| atccggagagt gcattccctgc ccactgcttt gagcgctccg gtctccgtgg tctctgccac | 360 |
| gttgccatcg atctgacttg ggctcgctc ttgttccctgg ctgcgaccctt gatcgacaag | 420 |
| tttgagaatc ctttgatccg ctatttggcc tggcctgtt actggatcat gcagggattt | 480 |
| gtctgcaccgg gtgtctgggt gctggctcac gagtgtggtc atcagtcctt ctcgacactcc | 540 |
| aagaccctca acaacacagt tgggtggatc ttgcactcga tgctcttggg cccctaccac | 600 |
| tcctggagaa tctcgactc gaagcaccac aaggccactg gccatatgac caaggaccag | 660 |
| gtctttgtgc ccaagaccgg ctcccagggtt ggcttgcttc ccaaggagaa cgctgctgct | 720 |
| gccgttcagg aggaggacat gtccgtgcac ctggatgagg aggctccat tggactttt | 780 |
| ttctggatgg tgatccagggtt cttgttcgga tggcccgctt acctgattat gaacgcctct | 840 |
| ggccaagact acggccgctg gacctcgac ttccacacgt actcgcccat ctttgagccc | 900 |
| cgcaacttt tcgacattat tatctcgac ctcgggtgtt tggctgccct cggtgccctg | 960 |
| atctatgcct ccatgcagggtt gtcgctctt accgtcacca agtactatat tggccctac | 1020 |
| ctctttgtca acttttgggtt ggtcctgatc accttcttgc agcacaccga tcccaagctg | 1080 |
| ccccattacc gcgagggtgc ctggaaatttc cagcgtggag ctcttgcac cgttgaccgc | 1140 |
| tctttggca agttcttggaa ccataatgttc cacggcattt tccacaccca tggccat | 1200 |
| cacttgttct cgcaaatttgc gtttaccat gctgagggaaat ctacctatca tctcaagaaaa | 1260 |
| ctgctggagat agtactatgtt gtacgaccctt tcccccgttgc tcgttgcgtt ctggaggatcg | 1320 |
| ttccgtgagt ggcgatttgtt ggaggatcatc ggagacgtgg tcttttcaa gaagtaaaaa | 1380 |
| aaaagacaat ggaccacaca caacccgttc tctacagacc tacgttatcat gtagccatac | 1440 |
| cacttcataa aagaacatga gctcttagagg cgtgtcatcc gcccctcc | 1488 |

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<211> 399

<212> PRT

<213> Mortierella alpina

<400> 4

Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
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Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
20 25 30

Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
35 40 45

His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
50 55 60

Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
65 70 75 80

Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
85 90 95

Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
100 105 110

Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
115 120 125

Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
130 135 140

Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
145 150 155 160

Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
165 170 175

Glu Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
180 185 190

Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
195 200 205

Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
210 215 220

Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
225 230 235 240

Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
245 250 255

Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
260 265 270

Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
275 280 285

Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr

290

295

300

Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
 305 310 315 320

Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
 325 330 335

Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
 340 345 350

Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
 355 360 365

Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
 370 375 380

Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
 385 390 395

<210> 5

<211> 355

<212> PRT

<213> Mortierella alpina

<400> 5

Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
 1 5 10 15

Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
 20 25 30

Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
 35 40 45

Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
 50 55 60

Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
 65 70 75 80

Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
 85 90 95

Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
 100 105 110

Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
 115 120 125

Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
 130 135 140

Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
 145 150 155 160

Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
 165 170 175

Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser

180

185

190

Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
195 200 205

His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
210 215 220

Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
225 230 235 240

Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
245 250 255

Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
260 265 270

Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
275 280 285

Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
290 295 300

His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
305 310 315 320

Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
325 330 335

Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
340 345 350

Lys Ala Gln
355

<210> 6
<211> 104
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (1)..(104)
<223> Amino acids 27, 48, and 63 uncertain of sequence

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Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
1 5 10 15

Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
20 25 30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
35 40 45

Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
50 55 60

Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp

| | | | |
|---|----|-----|-----|
| 65 | 70 | 75 | 80 |
| Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr | | | |
| 85 | | 90 | 95 |
| Gly Pro Asn Leu Gln His Ile Pro | | | |
| 100 | | | |
| <210> 7 | | | |
| <211> 252 | | | |
| <212> PRT | | | |
| <213> Arabidopsis thaliana | | | |
| <400> 7 | | | |
| Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln | | | |
| 1 | 5 | 10 | 15 |
| Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile | | | |
| 20 | | 25 | 30 |
| Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn | | | |
| 35 | 40 | | 45 |
| Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile | | | |
| 50 | 55 | | 60 |
| Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser | | | |
| 65 | 70 | 75 | 80 |
| Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser | | | |
| 85 | | 90 | 95 |
| Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu | | | |
| 100 | | 105 | 110 |
| Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr | | | |
| 115 | | 120 | 125 |
| Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr | | | |
| 130 | | 135 | 140 |
| Phe Leu Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn | | | |
| 145 | | 150 | 155 |
| 160 | | | |
| Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser | | | |
| 165 | | 170 | 175 |
| Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe | | | |
| 180 | | 185 | 190 |
| Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala | | | |
| 195 | | 200 | 205 |
| Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys | | | |
| 210 | | 215 | 220 |
| Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp | | | |
| 225 | | 230 | 235 |
| 240 | | | |
| Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His | | | |

245

250

<210> 8
<211> 125
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (1)..(125)
<223> Amino acids 2, 3, 30, 121, and 125 uncertain of sequence.

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Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
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Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
20 25 30

Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
35 40 45

Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
50 55 60

Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
65 70 75 80

Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
85 90 95

Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
100 105 110

Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
115 120 125

<210> 9
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (1)..(131)
<223> Amino acid at 110 uncertain of sequence

<400> 9

Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
1 5 10 15

Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
20 25 30

Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
35 40 45

Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
50 55 60

Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
65 70 75 80

Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
85 90 95

His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
100 105 110

Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
115 120 125

Lys Pro Leu
130

<210> 10

<211> 87

<212> PRT

<213> Caenorhabditis elegans

<400> 10

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
1 5 10 15

Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
20 25 30

Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
35 40 45

Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
65 70 75 80

Leu Val Gln Ala Lys Ala Ala
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<210> 11

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(143)

<223> Amino acid 125 uncertain of sequence

<400> 11

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1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
20 25 30

Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
35 40 45

Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
50 55 60

Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
65 70 75 80

Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
85 90 95

Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
100 105 110

His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
115 120 125

Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
130 135 140

<210> 12

<211> 35

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Description of Artificial Sequence: PCR Primer

<400> 12

ccaagttct gcaggagctc tttttttt tttt

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<210> 13

<211> 33

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 13

cuacuacuac uaggagtcc ctacggtgtt ttg

33

<210> 14

<211> 33

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 14
caucaucauc auatgatgct caagctgaaa ctg

33

<210> 15
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: PCR Primer

<400> 15
tacccaactcg agaaaaatggc tgctgctccc agtgtgagg

39

<210> 16
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 16
aactgatcta gattactgcg ccttaccat cttggaggc

39

<210> 17
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 17
tacccaactcg agaaaaatggc acctcccaac actatcgat

39

<210> 18
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 18
aactgatcta gattacttct tgaaaaagac cacgtctcc 39

<210> 19
<211> 746
<212> DNA
<213> Dictyostelium discoideum

<400> 19
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cactcctcta tggtatattac acactcaa atcgtactca agattggaa gctttgtaa 120
aggatggtaa aaatggtgca attcggtta gtgtcgccac aaatttcgat aaggccgctt 180
acgtcattgg taaaattgtct ttgttttct tccgtttcat ccttccactc cgttatcata 240
gctttacaga tttaatttgt tatttcctca ttgctgaatt cgtctttggg tggtatctca 300
caattaattt ccaagtttagt catgtcgctg aagatctcaa attctttgct acccctgaaa 360
gaccagatga accatctcaa atcaatgaag attgggcaat ccttcaactt aaaactactc 420
aagattatgg tcatggttca ctcccttgta ccttttttag tgggttctta aatcatcaag 480
ttgttcatca ttatttccca tcaattgctc aagatttcta cccacaactt gtaccaattg 540
taaaagaagt ttgtaaagaa cataacatta cttaccacat taaaccaa ac ttcaactgaag 600
ctattatgtc acacattaat tacctttaca aaatgggtaa tgatccagat tatgttaaaa 660
aaccattagc ctcaaaagat gattaaatga aataactaa aaaccaatta tttactttg 720
acaaacagta atattaataa atacaa 746

<210> 20
<211> 228
<212> PRT
<213> Dictyostelium discoideum

<220>
<221> UNSURE
<222> (1)..(228)
<223> Amino acid 228 uncertain of sequence

<400> 20

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln His
1 5 10 15

Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr Arg Thr
20 25 30

Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly Ala Ile Arg
35 40 45

Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr Val Ile Gly Lys

50

55

60

Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro Leu Arg Tyr His Ser
 65 70 75 80

Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile Ala Glu Phe Val Phe Gly
 85 90 95

Trp Tyr Leu Thr Ile Asn Phe Gln Val Ser His Val Ala Glu Asp Leu
 100 105 110

Lys Phe Phe Ala Thr Pro Glu Arg Pro Asp Glu Pro Ser Gln Ile Asn
 115 120 125

Glu Asp Trp Ala Ile Leu Gln Leu Lys Thr Thr Gln Asp Tyr Gly His
 130 135 140

Gly Ser Leu Leu Cys Thr Phe Phe Ser Gly Ser Leu Asn His Gln Val
 145 150 155 160

Val His His Leu Phe Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu
 165 170 175

Val Pro Ile Val Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His
 180 185 190

Ile Lys Pro Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu
 195 200 205

Tyr Lys Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser
 210 215 220

Lys Asp Asp Xaa
 225

<210> 21

<211> 494

<212> DNA

<213> Phaeodactylum tricorntatum

<220>

<221> misc_feature

<222> ()..()

<223> n at positions 11,20,29,31,40,53,453,489 may be a, c, g, or t

<400> 21

ttttggagg ntccaagttt accacggant nggcaagttt acggggcgga aancggtttt 60

ccccccaagc cttttgtcga ctgggtctgt ggtggcttcc agtaccaagt cgaccaccac 120

ttattcccca gcctgccccg acacaatctg gccaaagacac acgcacttgtt cgaatcgttc 180

tgcaaggagt ggggtgtcca gtaccacgaa gccgaccccg tggacgggac catgaaagtcc 240

ttgcaccatt tgggcagcgt ggccggcgaa ttcgtcggtt atttgtacg cgacggaccc 300

gccatgtaat cgtcgttgtt gacgatgcaa gggttcacgc acatctacac acactcactc 360

acacaacttag tgtaactcgt atagaattcg gtgtcgacct ggaccttggtt tgactgggtt 420

gggatagggt aggtaggcgg acgcgtgggt cgncccccggg aattctgtga ccggtacctg 480
gccccgcgtna aagt 494

<210> 22
<211> 102
<212> PRT
<213> Phaeodactylum tricornutum

<220>
<221> UNSURE
<222> (1)..(102)
<223> Amino acids 4,7,10,11,14, and 18 uncertain of sequence

<400> 22

Phe Trp Lys Xaa Pro Ser Xaa Pro Arg Xaa Xaa Gln Val Xaa Gly Ala
1 5 10 15

Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys Gly Gly
20 25 30

Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu Pro Arg His
35 40 45

Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe Cys Lys Glu Trp
50 55 60

Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp Gly Thr Met Glu Val
65 70 75 80

Leu His His Leu Gly Ser Val Ala Gly Glu Phe Val Val Asp Phe Val
85 90 95

Arg Asp Gly Pro Ala Met
100

<210> 23
<211> 520
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: Schizochytrium cDNA Clone

<400> 23
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cttgggtaca cgccggggca gtcgttgggc atgtacttgt gcgcctttgg tctcggctgc 120
atttacattt ttctgcagtt cgccgtaagt cacaccatt tgcccgtgag caacccggag 180
gatcagctgc attggctcga gtacgcgcgg accacactgt gaacatcagc accaagtctg 240
ggtttgcac atggtgatc tcgaacctca actttcagat cgagcaccac ctttccccca 300

cggcgccccca gttccgttcc aaggagatca gcccgcgcgt cgaggccctc ttcaagcgcc 360
acggtctccc ttactacgac atgccctaca cgagcgcgt ctccaccacc tttgccaacc 420
tctactccgt cggccattcc gtcggcgacg ccaagcgcga ctagcctt ttccttagacc 480
ttaattcccc accccacccc atgttctgtc ttccctccgc 520

<210> 24
<211> 153
<212> PRT
<213> Artificial/Unknown

<220>
<221> misc_feature
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<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 24

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys Arg
1 5 10 15

His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His Val Leu
20 25 30

Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala Val Arg Arg
35 40 45

Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly Ser Ala Ala Leu
50 55 60

Ala Arg Val Arg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp
65 70 75 80

Phe Val Thr Trp Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His
85 90 95

Leu Phe Pro Thr Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg
100 105 110

Val Glu Ala Leu Phe Lys Arg His Gly Leu Pro Tyr Tyr Asp Met Pro
115 120 125

Tyr Thr Ser Ala Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly
130 135 140

His Ser Val Gly Asp Ala Lys Arg Asp
145 150

<210> 25
<211> 420
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()...()
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 25
acgcgtccgc ccacgcgtcc gccgcgagca actcatcaag gaaggctact ttgacccttc 60
gctcccgcac atgacgtacc gcgtggtcga gattgttgc tcttcgtgc ttccctttg 120
gctgatgggt cagtcttcac ccctcgcgct cgctctcggc attgtcgtca gcggcatctc 180
tcagggtcgc tgccgctggg taatgcata gatgggcat gggtcgttca ctggtgtcat 240
ttggcttgac gaccgggtgt gcgagttctt ttacggcggtt ggttgtggca tgagcggtca 300
ttactggaaa aaccagcaca gcaaacacca cgcagcgcca aaccggctcg agcacatgt 360
agatctcaac accttgccat tggtggcctt caacgagcgc gtcgtgcga aggtccgacc 420

<210> 26
<211> 140
<212> PRT
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: Schizophyllum cDNA Clone

<400> 26

Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly Tyr
1 5 10 15

Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu Ile Val
20 25 30

Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser Ser Pro Leu
35 40 45

Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser Gln Gly Arg Cys
50 55 60

Gly Trp Val Met His Glu Met Gly His Gly Ser Phe Thr Gly Val Ile
65 70 75 80

Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe Tyr Gly Val Gly Cys Gly
85 90 95

Met Ser Gly His Tyr Trp Lys Asn Gln His Ser Lys His His Ala Ala
100 105 110

Pro Asn Arg Leu Glu His Asp Val Asp Leu Asn Thr Leu Pro Leu Val
115 120 125

Ala Phe Asn Glu Arg Val Val Arg Lys Val Arg Pro
130 135 140

<210> 27
<211> 1219
<212> DNA

<213> Homo sapiens

<400> 27

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| gcacggcggac | cgcgccggg | agatcctggc | aaagtatcca | gagataaaagt | ccttgatgaa | 60 |
| acctgatccc | aatttgcata | ttgattataat | tatgtatggtt | ctcacccagt | tgggtgcatt | 120 |
| ttacatagta | aaagacttgg | actggaaatg | ggtcataat | gggcctatg | cgtttggcag | 180 |
| ttgcattaac | cactcaatga | ctctggctat | tcatgagatt | gcccacaaatg | ctgccttgg | 240 |
| caactgcaaa | gcaatgtgga | atcgctggtt | tggaatgttt | gctaatcttc | ctattggat | 300 |
| tccatattca | atttccttta | agaggatata | catggatcat | catcggtacc | ttggagactga | 360 |
| tggcgctcgat | gtagatattc | ctacccgattt | tgagggctgg | ttcttctgt | ccgctttcag | 420 |
| aaagttata | tgggttattc | ttcagcctct | cttttatgcc | tttcgacctc | tgttcatcaa | 480 |
| ccccaaacca | attacgtatc | tggaagttat | caataccgtg | gcacaggtca | cttttgacat | 540 |
| ttaatttat | tacttttgg | gaattaaatc | cttagtctac | atgttggcag | catcttact | 600 |
| tggcctgggt | ttgcacccaa | tttctggaca | ttttatagct | gagcattaca | tgttcttaaa | 660 |
| gggtcatgaa | acttactcat | attatggcc | tctgaattt | cttaccttca | atgtgggtta | 720 |
| tcataatgaa | catcatgatt | tccccaacat | tcctggaaaa | agtcttccac | tggtagggaa | 780 |
| aatagcagct | gaatactatg | acaacccc | tcactacaat | tcctggataa | aagtactgt | 840 |
| tgattttgt | atggatgata | caataagtcc | ctactcaaga | atgaagaggg | accaaaaagg | 900 |
| agagatggtg | ctggagtaaa | tatcattagt | gccaaaggga | ttcttctcca | aaactttaga | 960 |
| tgataaaatg | gaattttgc | attattaaac | ttgagaccag | tgtgctcag | aagctcccct | 1020 |
| ggcacaattt | cagagtaaga | gctcggtat | accaagaagt | aatctggct | tttaaacagt | 1080 |
| cagcctgact | ctgtactgct | cagtttca | cacagggaaac | ttgtgacttg | tgtattatcg | 1140 |
| tcattgagga | tgtttcactc | atgtctgtca | ttttataaagc | atatcattt | aaaagcttct | 1200 |
| aaaaagctat | ttcgccagg | | | | | 1219 |

<210> 28

<211> 655

<212> DNA

<213> Homo sapiens

<400> 28

| | | | | | | |
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| ttaccttcta | cgtccgcttc | ttcctca | ttgtgccact | attggggctg | aaagcttcct | 60 |
| gggccttttc | ttcatagtc | ggttcctgg | aagcaactgg | tttgtgtggg | tgacacagat | 120 |
| gaaccatatt | cccatgcaca | ttgatcatga | ccggAACATG | gactgggtt | ccacccagct | 180 |
| ccaggccaca | tgcaatgtcc | acaagtctgc | cttcaatgac | tggttcagtg | gacacctaa | 240 |
| cttccagatt | gagcaccatc | ttttcccac | gatgcctcga | cacaattacc | acaaagtggc | 300 |

tccccctggtg cagtccttgt gtgccaaagca tggcatagag taccagtcca agcccctgct 360
gtcagcccttc gccgacatca tccactcaact aaaggagtca gggcagctct ggctagatgc 420
ctatcttac caataacaac agccaccctg cccagtcgtt aagaagagga ggaagactct 480
ggagccaaagg cagaggggag cttgagggac aatgccacta tagttaata ctcagagggg 540
gttgggtttt gggacataaaa gcctctgact caaactcctc ccttttatct tctagccaca 600
gttctaagac ccaaagtggg gggtggacac agaagtccct aggagggaaag gagct 655

<210> 29
<211> 304
<212> DNA
<213> Homo sapiens

<400> 29
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tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa 120
cccaagtgg aaccacttgt ccacaaattc gtcattggcc acttaaaggg tgccctcgcc 180
aactggtgga atcatcgcca cttccagcac cacgccaagg ctaacatctt ccacaaggat 240
cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc 300
aaga 304

<210> 30
<211> 918
<212> DNA
<213> Homo sapiens

<400> 30
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gagcgggtggc tagtgatcga ccgtaaggtg tacaacatca gcgagttcac ccggccggcat 120
ccagggggct cccgggtcat cagccactac gccgggcagg atgccacggg tccctttgtg 180
gccttccaca tcaacaaggg cttgtgaag aagtatatga actctctcct gattggagaa 240
ctgtctccag agcagcccaag cttgagccc accaagaata aagagctgac agatgagttc 300
cgggagctgc gggccacagt ggagcggatg gggctcatga aggccaacca tgtcttcttc 360
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tttgggacgt ctttttggc cttcctcctc tggcggtgc tgctcagtgc agttcaggcc 480
caggctggct ggctgcagca tgactttggg cacctgtcgg tcttcagcac ctcaaagtgg 540
aaccatctgc tacatcattt tgtgattggc cacctgaagg gggccccccgc cagttggtg 600
aaccacatgc acttccagca ccatgccaag cccaaactgct tccgcaaaga cccagacatc 660

| | | | | | | |
|-------------|--------------|-------------|------------|-------------|-------------|------|
| aacatgcata | ccttcttctt | tgccttgaaa | aagatcctct | ctgtggagct | tggaaacag | 720 |
| aagaaaaaat | atatgccgt | caaccaccag | cacaratact | tcttcctaatt | tggccccc | 780 |
| gccttgctgc | ctctctactt | ccagtggat | atttctatt | ttgttatcca | gcgaaagaag | 840 |
| tgggtggact | tggcctggat | cagcaaacag | gaatacgtat | aagccggct | tccattgtcc | 900 |
| accgcaaatg | cttctaaa | | | | | 918 |
| | | | | | | |
| <210> | 31 | | | | | |
| <211> | 1686 | | | | | |
| <212> | DNA | | | | | |
| <213> | Homo sapiens | | | | | |
| | | | | | | |
| <400> | 31 | | | | | |
| gccacttaaa | gggtgcctct | gc当地actgg | ggaatcatcg | ccacttccag | caccacgcca | 60 |
| agcctaaca | cttccacaag | gatcccgt | tgaacatgt | gcacgtgtt | gttctggcg | 120 |
| aatggcagcc | catcgagtac | ggcaagaaga | agctgaaata | cctgcctac | aatcaccagc | 180 |
| acgaaatactt | cttcctgatt | ggccgcccgc | tgctcatccc | catgtatttc | cagtaccaga | 240 |
| tcatcatgac | catgatcg | cataagaact | gggtggacct | ggcttggcc | gtcagctact | 300 |
| acatccgg | tttcatcacc | tacatccctt | tctacggcat | cctggagcc | ctcctttcc | 360 |
| tcaacttcat | cagg | tttgcact | gagaccact | gttttgttg | ggtcacacag | 420 |
| tcgtcatgga | gattgaccag | gaggcctacc | gtgactgg | cagtagccag | ctgacagcc | 480 |
| cctgcaacgt | ggagcagtcc | ttttcaacg | actggttcag | tggcacac | tttccaga | 540 |
| ttgagcacca | cctttcccc | accatgcccc | ggcacaactt | acacaagatc | gccccgtgg | 600 |
| tgaagtctct | atgtgccaag | catggcattt | aataccagga | gaagccgcta | ctgagggccc | 660 |
| tgctggacat | catcagg | ctgaagaagt | ctggaaagct | gtggctgg | gcctac | 720 |
| acaaatgaag | ccacagcccc | cggacaccg | tggggaaagg | gtgcagg | gtgtatggcc | 780 |
| agaggaatga | tgggtttt | ttctgaggg | tgtccgagag | gctgggtat | gcactgctca | 840 |
| cggacccat | gttggatctt | tctcccttc | tcctctc | tttctttca | catctcccc | 900 |
| atagcaccc | gccctcatgg | gacctgcct | ccctcagcc | tcagccatca | gccatggccc | 960 |
| tcccagtgcc | tcctagcccc | ttttccaag | gagcagag | gtggccaccg | gggggtggctc | 1020 |
| tgtcctac | ccactctctg | cccctaaaga | tgggaggaga | ccagcgg | atgggtctgg | 1080 |
| cctgtgagtc | tcccttgca | gcctgg | taggcattac | ccccgtttt | gttcttcaga | 1140 |
| tgctcttggg | gttcataggg | gcaggtccta | gtcgggcagg | gcccctgacc | ctcccggcct | 1200 |
| ggcttcactc | tccctgacgg | ctgcccattgg | tccaccc | tttcatagagg | cctgcttgt | 1260 |
| tacaaagctc | gggtctccct | cctgcagctc | ggttaagtac | ccgaggcctc | tcttaagatg | 1320 |

| | | | |
|------------------------|-----------------------|------------------------|------|
| tccagggccc caggccccg | ggcacagcca gccaaacct | tggccctgg aagagtcc | 1380 |
| caccccatca ctagagtgt | ctgaccctgg gcttcacgg | gccccattcc accgcctccc | 1440 |
| caacttgagc ctgtgacctt | gggaccaaag gggagtc | ccctgtcttg tgactcagca | 1500 |
| gaggcagtgg ccacgttcag | ggagggccc | gctggccctgg aggctcagcc | 1560 |
| ctttcctca gggtgtcctg | aggtccaaga ttctggagca | atctgaccct tctccaaagg | 1620 |
| ctctgttatac agctgggcag | tgccagccaa tccctggcca | tttggcccca ggggacgtgg | 1680 |
| gccctg | | | 1686 |

<210> 32
<211> 1843
<212> DNA
<213> Homo sapiens

| | | | |
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| tctcaggccc aagctggatg | gctgcaacat gattatggcc | acctgtctgt ctacagaaaa | 120 |
| cccaagtggaa accacttgt | ccacaattc gtcattggcc | acttaaaggg tgcctctgcc | 180 |
| aactggtgga atcatcgcca | cttccagcac cacgccaagc | ctaacatctt ccacaaggat | 240 |
| cccgatgtga acatgctgca | cgtgtttgtt ctggcgaat | ggcagcccat cgagtacggc | 300 |
| aagaagaagc tgaaatacct | gccctacaat caccagcacg | aataacttctt cctgattggg | 360 |
| ccgcccgtgc tcatccccat | gtattccag taccagatca | tcatgaccat gatcgccat | 420 |
| aagaactggg tggacctggc | ctggccgtc agtactaca | tccggttctt catcacctac | 480 |
| atccctttct acggcatcct | gggagccctc ctttcctca | acttcatcag gttcctggag | 540 |
| agccactggt ttgtgtgggt | cacacagatg aatcacatcg | tcatggagat tgaccaggag | 600 |
| gcctaccgtg actgggttcag | tagccagctg acagccacct | gcaacgtggc gcagtccttc | 660 |
| ttcaacgact gttcagtgg | acacctaacttcc | ttccagattt agcaccacct | 720 |
| atgccccggc acaacttaca | caagatcgcc | ccgctgggtga agtctctatg tgccaaagcat | 780 |
| ggcattgaat accaggagaa | gccgctactg | agggccctgc tggacatcat | 840 |
| aagaagtctg ggaagctgtg | gctggacgccc | taccttcaca aatgaagcca | 900 |
| gacaccgtgg ggaagggggtg | caggtgggggt | gatggccaga ggaatgatgg | 960 |
| tgaggggtgt ccgagaggct | ggtgtatgca | ctgctcacgg accccatgtt | 1020 |
| ccctttctcc tctcctttt | ctcttcacat | ctccccata gcaccctgcc | 1080 |
| ctgcccctccc tcagccgtca | gccatcagcc | atggccctcc cagtgccctcc | 1140 |
| ttccaaggag cagagagggtg | gccaccgggg | gtggctctgt cctacacttca | 1200 |

| | | | | | | |
|------------|-------------|--------------|-------------|------------|------------|------|
| ctaaagatgg | gaggagacca | gcggtccatg | ggtctggcct | gtgagtctcc | cttgcagcc | 1260 |
| tggtaactag | gcatcacccc | cgcttgggtt | cttcagatgc | tcttggggtt | cataggggca | 1320 |
| ggtcctagtc | gggcagggcc | cctgaccctc | ccggcctggc | ttcactctcc | ctgacggctg | 1380 |
| ccattggtcc | accctttcat | agagaggcct | gctttgttac | aaagctcggg | tctccctcct | 1440 |
| gcagctcggt | taagtacccg | aggcctctct | taagatgtcc | agggccccag | gcccgcgggc | 1500 |
| acagccagcc | caaaccctgg | gcccttggaaag | agtccctccac | cccatcacta | gagtgctctg | 1560 |
| accctgggct | ttcacgggccc | ccattccacc | gcctcccaa | cttgcgcctg | tgaccttggg | 1620 |
| accaaagggg | gagtccctcg | tctcttgtga | ctcagcagag | gcagtggcca | cgttcaggga | 1680 |
| ggggccggct | ggcctggagg | ctcagccac | cctccagctt | ttcctcaggg | tgtcctgagg | 1740 |
| tccaagattc | tggagcaatc | tgacccttct | ccaaaggctc | tgttatcagc | tgggcagtc | 1800 |
| cagccaatcc | ctggccattt | ggcccccaggg | gacgtgggccc | ctg | | 1843 |

<210> 33
 <211> 2257
 <212> DNA
 <213> Homo sapiens

| | | | | | | |
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| <400> 33 | | | | | | |
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| gagcggtggc | tagtgcata | ccgtaaggtg | tacaacatca | gcgagttcac | ccgcccggcat | 120 |
| ccagggggct | cccggtcat | cagccactac | gccgggcagg | atgccacgga | tccctttgtg | 180 |
| gccttccaca | tcaacaaggg | ccttgtgaag | aagtatatga | actctctcct | gattggagaa | 240 |
| ctgtctccag | agcagccacag | cttgagcccc | accaagaata | aagagctgac | agatgagttc | 300 |
| cgggagctgc | gggccacagt | ggagcgatg | gggctcatga | aggccaacca | tgtcttcttc | 360 |
| ctgctgtacc | tgctgcacat | cttgctgctg | gatggtgcag | cctggctcac | cctttgggtc | 420 |
| tttgggacgt | cctttttgcc | cttcctccctc | tgtgcgggtgc | tgctcagtgc | agttcagcag | 480 |
| gccccagctg | gatggctgca | acatgattat | ggccacctgt | ctgtctacag | aaaacccaag | 540 |
| tggaaccacc | ttgtccacaa | attcgtcatt | ggccacttaa | agggtgcctc | tgccaaactgg | 600 |
| tggaatcatc | gccacttcca | gcaccacgccc | aagcctaaca | tcttccacaa | ggatcccgat | 660 |
| gtgaacatgc | tgcacgtgtt | tgttctgggc | aatggcagc | ccatcgagta | cgccaagaag | 720 |
| aagctgaaat | acctgcctta | caatcaccag | cacgaatact | tcttcctgtat | tgggcccgg | 780 |
| ctgctcatcc | ccatgtat | ccagtagcc | atcatcatga | ccatgatcgt | ccataagaac | 840 |
| tgggtggacc | tggcctgggc | cgtcagctac | tacatccggt | tcttcatcac | ctacatccct | 900 |
| ttctacggca | tcctgggagc | cctccttttc | ctcaacttca | tcaggttcct | ggagagccac | 960 |

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|------|
| tggtttgtt | gggtcacaca | gatgaatcac | atcgcatgg | agattgacca | ggaggcctac | 1020 |
| cgtgactgg | ttagtagcca | gctgacagcc | acctgcaacg | tggagcagtc | cttcttcaac | 1080 |
| gactggttca | gtggacaccc | taacttccag | attgagcacc | accttccc | caccatgcc | 1140 |
| cggcacaact | tacacaagat | cgcggcgtg | gtgaagtctc | tatgtccaa | gcatggcatt | 1200 |
| gaataccagg | agaagccgct | actgagggcc | ctgctggaca | tcatcaggc | cctgaagaag | 1260 |
| tctgggaagc | tgtggctgga | cgcctaccc | cacaaatgaa | gccacagccc | ccgggacacc | 1320 |
| gtggggaaagg | ggtgcagg | gggtgatggc | cagaggaatg | atgggctttt | gttctgaggg | 1380 |
| gtgtccgaga | ggctggtgta | tgcactgctc | acggacccc | tgttggatct | ttctccctt | 1440 |
| ctcctctcct | tttctcttc | acatctcccc | catagcaccc | tgcctcatg | ggacctgccc | 1500 |
| tccctcagcc | gtcagccatc | agccatggcc | ctcccaagtgc | ctcctagccc | cttctccaa | 1560 |
| ggagcagaga | ggtggccacc | gggggtggct | ctgtcctacc | tccactctct | gcccctaag | 1620 |
| atgggaggag | accagcggc | catgggtctg | gcctgtgagt | ctcccttgc | agcctggc | 1680 |
| ctaggcatca | cccccgctt | gttcttcag | atgctcttgg | gttcataagg | ggcaggcct | 1740 |
| atcggggcag | ggcccctgac | cctccggcc | tggcttact | ctccctgacg | gctgccattg | 1800 |
| gtccaccctt | tcatagagag | gcctgctttt | ttacaaagct | cgggtctccc | tcctgcagct | 1860 |
| cggtaagta | cccgaggcct | ctcttaagat | gtccagggcc | ccaggcccgc | gggcacagcc | 1920 |
| agcccaaacc | ttggggccctg | gaagagtcct | ccacccatc | actagagtgc | tctgaccctg | 1980 |
| ggcttcacg | ggccccattc | caccgcctcc | ccaaacttgc | cctgtgaccc | tgggaccaaa | 2040 |
| gggggagtcc | ctcgctcttt | gtgactcagc | agaggcagtg | gccacgttca | gggagggcc | 2100 |
| ggctggcctg | gaggctcagc | ccacccctca | gctttcctc | agggtgtctt | gaggtc当地 | 2160 |
| attctggagc | aatctgaccc | ttctccaaag | gctctgttat | cagctggca | gtgccagcc | 2220 |
| atccctggcc | atttggccccc | agggacgtg | ggccctg | | | 2257 |

<210> 34
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (1)..(406)
 <223> Amino acids 306,329,331,334,358,375, and 382 uncertain of sequence

<400> 34

His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile Lys
 1 5 10 15

Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile Met Met
20 25 30

Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp Leu Asp Trp
35 40 45

Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser Cys Ile Asn His
50 55 60

Ser Met Thr Leu Ala Ile His Glu Ile Ala His Asn Ala Ala Phe Gly
65 70 75 80

Asn Cys Lys Ala Met Trp Asn Arg Trp Phe Gly Met Phe Ala Asn Leu
85 90 95

Pro Ile Gly Ile Pro Tyr Ser Ile Ser Phe Lys Arg Tyr His Met Asp
100 105 110

His His Arg Tyr Leu Gly Ala Asp Gly Val Asp Val Asp Ile Pro Thr
115 120 125

Asp Phe Glu Gly Trp Phe Phe Cys Thr Ala Phe Arg Lys Phe Ile Trp
130 135 140

Val Ile Leu Gln Pro Leu Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn
145 150 155 160

Pro Lys Pro Ile Thr Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val
165 170 175

Thr Phe Asp Ile Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val
180 185 190

Tyr Met Leu Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser
195 200 205

Gly His Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr
210 215 220

Tyr Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
225 230 235 240

His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu Pro
245 250 255

Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro His Tyr
260 265 270

Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp Asp Thr Ile
275 280 285

Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly Glu Met Val Leu
290 295 300

Glu Xaa Ile Ser Leu Val Pro Lys Gly Phe Phe Ser Lys Thr Leu Asp
305 310 315 320

Asp Lys Met Glu Phe Leu His Tyr Xaa Thr Xaa Asp Gln Xaa Cys Ser
325 330 335

Glu Ala Pro Leu Ala Gln Phe Gln Ser Lys Ser Ser Val Ile Pro Arg

340

345

350

Ser Glu Ser Gly Phe Xaa Thr Val Ser Leu Thr Leu Tyr Cys Ser Val
355 360 365

Ser Leu Thr Gly Asn Leu Xaa Leu Val Tyr Tyr Arg His Xaa Gly Cys
370 375 380

Phe Thr His Val Cys His Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu
 385 390 395 400

Lys Ser Tyr Phe Ala Arg
405

<210> 35

<211> 218

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1) .. (218)

<223> Amino acids 145, 168, 174, 186, 189, 198, and 202 uncertain of sequence

<400> 35

Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly Ala
1 5 10 15

Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn
20 25 30

Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met His Ile Asp
35 40 45

His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys
50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | His | Lys | Ser | Ala | Phe | Asn | Asp | Trp | Phe | Ser | Gly | His | Leu | Asn |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |

Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr
85 90 . . 95

His Lys Val Ala Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile
100 105 110

Glu Tyr Gln Ser Lys Pro Leu Leu Ser Ala Phe Ala Asp Ile Ile His
115 . 120 125

Ser Leu Lys Glu Ser Gly Gln Leu Trp Leu Asp Ala Tyr Leu His Gln
130 135 140

Xaa Gln Gln Pro Pro Cys Pro Val Trp Lys Lys Arg Arg Lys Thr Leu
145 . . . 150 155 . . . 160

Glu Pro Arg Gln Arg Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn
165 170 175

Thr Gln Arg Gly Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu
180 185 190

Leu Pro Phe Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val
195 200 205

Asp Thr Glu Val Pro Arg Arg Glu Gly Ala
210 215

<210> 36

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(87)

<223> Amino acid 87 uncertain of sequence

<400> 36

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Leu Gly Glu Trp Gln
65 70 75 80

Pro Ile Glu Tyr Gly Lys Xaa
85

<210> 37

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(306)

<223> Amino acid 252 uncertain of sequence

<400> 37

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser

35

40

45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile
 50 55 60

Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu
 65 70 75 80

Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu
 85 90 95

Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu
 100 105 110

Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu
 115 120 125

Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser
 130 135 140

Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala
 145 150 155 160

Gln Ala Gly Trp Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser
 165 170 175

Thr Ser Lys Trp Asn His Leu Leu His His Phe Val Ile Gly His Leu
 180 185 190

Lys Gly Ala Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His
 195 200 205

Ala Lys Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro
 210 215 220

Phe Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
 225 230 235 240

Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe Leu
 245 250 255

Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr Ile Phe
 260 265 270

Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala Trp Ile Ser
 275 280 285

Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser Thr Ala Asn Ala
 290 295 300

Ser Lys
 305

<210> 38
 <211> 562
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (1)...(562)

<223> Amino acids 242, 268, 405, 438, 464, 482, 497, and 562 uncertain of sequence

<400> 38

His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln
1 5 10 15

His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met
20 25 30

Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys
35 40 45

Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe
50 55 60

Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile
65 70 75 80

Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala
85 90 95

Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
100 105 110

Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser
115 120 125

His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile
130 135 140

Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr
145 150 155 160

Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu
165 170 175

Asn Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
180 185 190

Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly
195 200 205

Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile
210 215 220

Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
225 230 235 240

Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp
245 250 255

Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu
260 265 270

Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro
275 280 285

Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro

290

295

300

Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu
 305 310 315 320

Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro
 325 330 335

Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly
 340 345 350

Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp
 355 360 365

Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe
 370 375 380

Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp
 385 390 395 400

Leu His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg
 405 410 415

Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser
 420 425 430

Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr
 435 440 445

Ala Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa
 450 455 460

Ser Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 465 470 475 480

Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu
 485 490 495

Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro
 500 505 510

Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser
 515 520 525

Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala
 530 535 540

Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly
 545 550 555 560

Pro Xaa

<210> 39

<211> 615

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)...(615)

<223> Amino acids 295, 321, 458, 491, 517, 535, 550, and 615 uncertain of sequence

<400> 39

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp
65 70 75 80

Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro
85 90 95

Ile Glu Tyr Gly Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln
100 105 110

His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
115 120 125

Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val
130 135 140

Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr
145 150 155 160

Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile
165 170 175

Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His
180 185 190

Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser
195 200 205

Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp
210 215 220

Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
225 230 235 240

Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu
245 250 255

Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala
260 265 270

Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu
275 280 285

Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly

290

295

300

Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe
 305 310 315 320

Xaa Gly Val Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met
 325 330 335

Leu Asp Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro
 340 345 350

His Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
 355 360 365

Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala
 370 375 380

Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro
 385 390 395 400

Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser
 405 410 415

Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln
 420 425 430

Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu
 435 440 445

Thr Leu Pro Ala Trp Leu His Ser Pro Xaa Arg Leu Pro Leu Val His
 450 455 460

Pro Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
 465 470 475 480

Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro
 485 490 495

Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro
 500 505 510

Pro Pro His His Xaa Ser Ala Leu Thr Leu Gly Phe His Gly Pro His
 515 520 525

Ser Thr Ala Ser Pro Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly
 530 535 540

Val Pro Arg Leu Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly
 545 550 555 560

Gly Ala Gly Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln
 565 570 575

Gly Val Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys
 580 585 590

Ala Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 595 600 605

Pro Gly Asp Val Gly Pro Xaa
 610 615

<210> 40
<211> 753
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (1)..(753)
<223> Amino acids 433,459,596,629,655,673,688, and 753 uncertain of sequence

<400> 40

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser
35 40 45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile
50 55 60

Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu
65 70 75 80

Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu
85 90 95

Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu
100 105 110

Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu
115 120 125

Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser
130 135 140

Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Gln
145 150 155 160

Ala Gln Ala Gly Trp Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr
165 170 175

Arg Lys Pro Lys Trp Asn His Leu Val His Lys Phe Val Ile Gly His
180 185 190

Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His
195 200 205

His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu
210 215 220

His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys
225 230 235 240

Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu
245 250 255

Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile
260 265 270

Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
275 280 285

Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile
290 295 300

Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His
305 310 315 320

Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp
325 330 335

Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys
340 345 350

Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn
355 360 365

Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu
370 375 380

His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile
385 390 395 400

Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
405 410 415

Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
420 425 430

Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly
435 440 445

Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg
450 455 460

Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe
465 470 475 480

Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser
485 490 495

Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro
500 505 510

Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly
515 520 525

Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly Asp
530 535 540

Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp Ser
545 550 555 560

Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe Ile
565 570 575

Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu
580 585 590

His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro
595 600 605

Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr
610 615 620

Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala
625 630 635 640

Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
645 650 655

Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr
660 665 670

Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa
675 680 685

Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly
690 695 700

Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
705 710 715 720

Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly
725 730 735

Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro
740 745 750

Xaa

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